Blast 2 Sequences results

(iv)

NCBI

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May–07–2006]
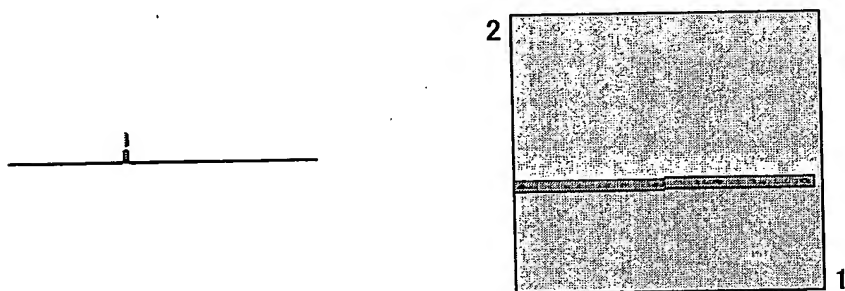
Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide   Masking color option Black
☐ Show CDS translation   Align

Sequence 1: lcl|1_seq_1
Length = 31 (1 .. 31)

Sequence 2: lcl|2_seq_2
Length = 4258 (1 .. 4258)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 60.3 bits (31),  Expect = 1e-07
 Identities = 31/31 (100%), Gaps = 0/31 (0%)
 Strand=Plus/Plus

Query  1     AAGCCGACTTCCAGATCTACTCGGAGTACTG  31
             |||||||||||||||||||||||||||||||
Sbjct  1626  AAGCCGACTTCCAGATCTACTCGGAGTACTG  1656
```

CPU time: 0.01 user secs.   0.00 sys. secs   0.01 total secs.

Lambda   K   H
 1.33   0.621   1.12

Gapped
Lambda   K   H
 1.33   0.621   1.12

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Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1

Blast Result

Number of Hits to DB: 7
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 31
Length of database: 18,725,440,322
Length adjustment: 22
Effective length of query: 9
Effective length of database: 18,725,440,300
Effective search space: 168528962700
Effective search space used: 168528962700
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 18 (35.3 bits)